

PCT09

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/869,564

TIME: 13:57:31

Input Set : A:\59367.app

Output Set: N:\CRF3\11142001\I869564.raw

3 <110> APPLICANT: Markham and Bonthron
 5 <120> TITLE OF INVENTION: Wound Healing and Orofacial Clefting
 7 <130> FILE REFERENCE: 59367
 9 <140> CURRENT APPLICATION NUMBER: 09/869,564
 10 <141> CURRENT FILING DATE: 2001-06-29
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB00/00003
 13 <151> PRIOR FILING DATE: 2000-01-06
 15 <150> PRIOR APPLICATION NUMBER: GB9900167.9
 16 <151> PRIOR FILING DATE: 1999-01-06
 18 <160> NUMBER OF SEQ ID NOS: 39
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4997
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (85)..(2283)
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 34 actttgtctc cgagtcggag cagc atg gag cgg cgg agc gag agc ccg tgt 111
 35 Met Glu Arg Arg Ser Glu Ser Pro Cys
 36 1 5
 38 ctg cgg gac agc ccc gac cgg cgg agc ggc agc ccg gac gtc aag ggg 159
 39 Leu Arg Asp Ser Pro Asp Arg Arg Ser Gly Ser Pro Asp Val Lys Gly
 40 10 15 20 25
 42 cct ccc cca gtg aag gtg gcc cgg ctg gag cag aac ggc agc ccc atg 207
 43 Pro Pro Pro Val Lys Val Ala Arg Leu Glu Gln Asn Gly Ser Pro Met
 44 30 35 40
 46 gga gcc cgc ggg agg ccc aac ggc gcc gtg gcc aag gcc gtg gga ggt 255
 47 Gly Ala Arg Gly Arg Pro Asn Gly Ala Val Ala Lys Ala Val Gly Gly
 48 45 50 55
 50 ttg atg att cct gtc ttt tgt gtc gtg gag cag ttg gac ggc tct ctt 303
 51 Leu Met Ile Pro Val Phe Cys Val Val Glu Gln Leu Asp Gly Ser Leu
 52 60 65 70
 54 gaa tat gac aac aga gaa gaa cac gcc gag ttt gtc ctg gtg cgg aaa 351
 55 Glu Tyr Asp Asn Arg Glu Glu His Ala Glu Phe Val Leu Val Arg Lys
 56 75 80 85
 58 gat gtg ctt ttt agc cag ctg gtg gag act gcg ctc ctg gcc ctg ggg 399
 59 Asp Val Leu Phe Ser Gln Leu Val Glu Thr Ala Leu Leu Ala Leu Gly
 60 90 95 100 105
 62 tat tct cac agc tct gcg gcc cag gcc caa gga ata atc aag ctg gga 447
 63 Tyr Ser His Ser Ser Ala Ala Gln Ala Gln Gly Ile Ile Lys Leu Gly
 64 110 115 120
 66 agg tgg aac cct ctc ccc ctc agt tat gtg aca gat gca ccc gac gcg 495
 67 Arg Trp Asn Pro Leu Pro Leu Ser Tyr Val Thr Asp Ala Pro Asp Ala
 68 125 130 135

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p. 5

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70 aca gtg gcc gac atg cta caa gat gtc tat cat gtt gtg acg ttg aaa 543
71 Thr Val Ala Asp Met Leu Gln Asp Val Tyr His Val Val Thr Leu Lys
72      140      145      150
74 atc caa tta caa agt tgt tca aag ttg gaa gac ttg cct gcg gag cag 591
75 Ile Gln Leu Gln Ser Cys Ser Lys Leu Glu Asp Leu Pro Ala Glu Gln
76      155      160      165
78 tgg aac cat gcc aca gtc cgc aat gcc tta aag gaa ctg ctc aaa gag 639
79 Trp Asn His Ala Thr Val Arg Asn Ala Leu Lys Glu Leu Leu Lys Glu
80 170      175      180      185
82 atg aac cag agc aca tta gcc aaa gaa tgc cct ctc tcc cag agt atg 687
83 Met Asn Gln Ser Thr Leu Ala Lys Glu Cys Pro Leu Ser Gln Ser Met
84      190      195      200
86 att tca tcc att gta aat agc aca tat tat gcc aat gtg tca gca acc 735
87 Ile Ser Ser Ile Val Asn Ser Thr Tyr Tyr Ala Asn Val Ser Ala Thr
88      205      210      215
90 aag tgc cag gag ttt ggg aga tgg tat aaa aag tac aag aag att aaa 783
91 Lys Cys Gln Glu Phe Gly Arg Trp Tyr Lys Lys Tyr Lys Lys Ile Lys
92      220      225      230
94 gtg gaa aga gtg gaa cga gaa aac ctt tca gac tat tgt gtt ctg ggc 831
95 Val Glu Arg Val Glu Arg Glu Asn Leu Ser Asp Tyr Cys Val Leu Gly
96      235      240      245
98 cag cgt cca atg cat tta cca aat atg aac cag ctg gca tcc ctg ggg 879
99 Gln Arg Pro Met His Leu Pro Asn Met Asn Gln Leu Ala Ser Leu Gly
100 250      255      260      265
102 aaa acc aac gaa cag tct cct cac agc caa att cac cac agt act cca 927
103 Lys Thr Asn Glu Gln Ser Pro His Ser Gln Ile His His Ser Thr Pro
104      270      275      280
106 atc cga aac caa gtg ccc gca tta cag ccc atc atg agc cct ggt ctt 975
107 Ile Arg Asn Gln Val Pro Ala Leu Gln Pro Ile Met Ser Pro Gly Leu
108      285      290      295
110 ctt tct ccc cag ctt agt cca caa ctt gta agg caa caa ata gcc atg 1023
111 Leu Ser Pro Gln Leu Ser Pro Gln Leu Val Arg Gln Gln Ile Ala Met
112      300      305      310
114 gcc cat ctg ata aac caa cag att gcc gtt agc cgg ctc ctg gct cac 1071
115 Ala His Leu Ile Asn Gln Gln Ile Ala Val Ser Arg Leu Leu Ala His
116      315      320      325
118 cag cat cct caa gcc atc aac cag cag ttc ctg aac cat cca ccc atc 1119
119 Gln His Pro Gln Ala Ile Asn Gln Gln Phe Leu Asn His Pro Pro Ile
120 330      335      340      345
122 ccc aga gca gtt aag cca gag cca acc aac tct tcc gtg gaa gtc tct 1167
123 Pro Arg Ala Val Lys Pro Glu Pro Thr Asn Ser Ser Val Glu Val Ser
124      350      355      360
126 cca gat atc tac cag caa gtc aga gat gag ctg aag agg gcc agt gtg 1215
127 Pro Asp Ile Tyr Gln Gln Val Arg Asp Glu Leu Lys Arg Ala Ser Val
128      365      370      375
130 tcc caa gct gtc ttt gca aga gtg gca ttc aac cgc aca cag gga ttg 1263
131 Ser Gln Ala Val Phe Ala Arg Val Ala Phe Asn Arg Thr Gln Gly Leu
132      380      385      390
134 ttg tct gag att ctg cgt aag gaa gaa gac cct cgg aca gcc tct cag 1311

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135 Leu Ser Glu Ile Leu Arg Lys Glu Glu Asp Pro Arg Thr Ala Ser Gln
136      395      400      405
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139 Ser Leu Leu Val Asn Leu Arg Ala Met Gln Asn Phe Leu Asn Leu Pro
140 410      415      420      425
142 gaa gtg gag cga gat cgc atc tac cag gat gag agg gag cgg agc atg 1407
143 Glu Val Glu Arg Asp Arg Ile Tyr Gln Asp Glu Arg Glu Arg Ser Met
144      430      435      440
146 aat ccc aat gtg agc atg gtc tcc tcg gcc tcc agc agt ccc agc tcc 1455
147 Asn Pro Asn Val Ser Met Val Ser Ser Ala Ser Ser Ser Pro Ser Ser
148      445      450      455
150 tcc cga acc cct cag gcc aaa acc tcg aca ccg aca aca gac ctc cct 1503
151 Ser Arg Thr Pro Gln Ala Lys Thr Ser Thr Pro Thr Thr Asp Leu Pro
152      460      465      470
154 att aag gtg gac ggc gcc aac atc aac atc aca gct gcc att tat gac 1551
155 Ile Lys Val Asp Gly Ala Asn Ile Asn Ile Thr Ala Ala Ile Tyr Asp
156      475      480      485
158 gag atc caa cag gag atg aaa agg gcc aag gtg tct caa gcc ctg ttt 1599
159 Glu Ile Gln Gln Glu Met Lys Arg Ala Lys Val Ser Gln Ala Leu Phe
160 490      495      500      505
162 gcc aaa gtg gct gca aat aaa agt cag ggc tgg ctg tgt gaa ctg ctc 1647
163 Ala Lys Val Ala Ala Asn Lys Ser Gln Gly Trp Leu Cys Glu Leu Leu
164      510      515      520
166 cgc tgg aag gag aac cca agc cca gaa aac cgc acc ctc tgg gaa aac 1695
167 Arg Trp Lys Glu Asn Pro Ser Pro Glu Asn Arg Thr Leu Trp Glu Asn
168      525      530      535
170 ctc tgt acc atc cgt cgc ttc ctg aac ctt ccc cag cat gag agg gat 1743
171 Leu Cys Thr Ile Arg Arg Phe Leu Asn Leu Pro Gln His Glu Arg Asp
172      540      545      550
174 gtc atc tat gag gag gag tca agg cat cac cac agc gaa cgc atg caa 1791
175 Val Ile Tyr Glu Glu Glu Ser Arg His His His Ser Glu Arg Met Gln
176      555      560      565
178 cac gtg gtc cag ctt ccc cct gag ccg gtg cag gta ctt cat aga cag 1839
179 His Val Val Gln Leu Pro Glu Pro Val Gln Val Leu His Arg Gln
180 570      575      580      585
182 cag tct cag cca gcc aag gag agt tcc cct ccc aga gaa gaa gcg cct 1887
183 Gln Ser Gln Pro Ala Lys Glu Ser Ser Pro Pro Arg Glu Glu Ala Pro
184      590      595      600
186 ccc cca cct cct ccg act gaa gac agt tgt gcc aaa aag ccc cgg tct 1935
187 Pro Pro Pro Pro Pro Thr Glu Asp Ser Cys Ala Lys Lys Pro Arg Ser
188      605      610      615
190 cgc aca aag atc tcc tta gaa gcc ctg ggg atc ctc caa agc ttt att 1983
191 Arg Thr Lys Ile Ser Leu Glu Ala Leu Gly Ile Leu Gln Ser Phe Ile
192      620      625      630
194 cat gat gta ggc ctg tac cca gac cag gaa gcc atc cac act ctt tcg 2031
195 His Asp Val Gly Leu Tyr Pro Asp Gln Glu Ala Ile His Thr Leu Ser
196      635      640      645
198 gct cag ctg gat ctc ccc aaa cac acc atc atc aag ttc ttc cag aac 2079
199 Ala Gln Leu Asp Leu Pro Lys His Thr Ile Ile Lys Phe Phe Gln Asn

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200 650                               655                               660                               665
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203 Gln Arg Tyr His Val Lys His His Gly Lys Leu Lys Glu His Leu Gly
204                               670                               675                               680
206 tcc gcg gtg gac gtg gct gaa tat aag gac gag gag ctg ctg acc gag 2175
207 Ser Ala Val Asp Val Ala Glu Tyr Lys Asp Glu Glu Leu Leu Thr Glu
208                               685                               690                               695
210 tca gag gag aac gac agc gag gaa ggc tcc gag gag atg tac aaa gtg 2223
211 Ser Glu Glu Asn Asp Ser Glu Glu Gly Ser Glu Glu Met Tyr Lys Val
212                               700                               705                               710
214 gag gct gag gag gaa aat gct gac aaa agc aag gca gca cct gcc gaa 2271
215 Glu Ala Glu Glu Glu Asn Ala Asp Lys Ser Lys Ala Ala Pro Ala Glu
216                               715                               720                               725
218 att gac cag aga taatgtgaac ttctactagg caaagcaata catcggtcca 2323
219 Ile Asp Gln Arg
220 730
222 aggatTTTTct gctttcattt ctttaaaagt tttttgttag tttgtTTTTt gtttttgttt 2383
224 ttgggtTTTTt ttggctttat ttttgtcttt ttatgtctgt tttgtTTTTc ttaccctttt 2443
226 ggacattttct ttgttgacac ggatacacct atagactgaa taagttcagt atttcogaat 2503
228 cagacatcgc cttggcaaaag acactaaagc gttacacttt atcccgtctc tatgactgga 2563
230 tcatagtcac tataatcaca ggagactctg ccttcattat ccttgcactt aacggaagtt 2623
232 acatcaggca agttccagga tgaaaagaac tatgaaataa atgaagggaag ctacaagtgt 2683
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246 ggcacattaa aatgatacaa gtcaaataaa tcttaaagac acaatgcaca cttaaaatga 3103
248 ctcaataaaa tgacttgcta cgttccgtta ttcaatttgt cactactgta gtgaacagat 3163
250 gcattttctgt ggaattccaa ataagtaaaa ctgaaattca gtgcagagaa aactttgtcc 3223
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254 agccacattt tgttgtgaaa tttatttacc tgcttggtggc ttcaaactcg aaaattaata 3343
256 agcctgctcg tttaaaagtt gtttggttgt gctgtttttt tgtctttttg ttttttacta 3403
258 gaaaatagtt cagtgttaata ttaagttaga aaagaagttg ctgcccagtt aaaggggctc 3463
260 cctctcaaat aaatctccat ccttccctct cccaaaagac atttctgatt tctgcttcac 3523
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266 tgcagctcca ggcaatagag tatgtgaagc gatttcagta gaatcactta ctcatcctaa 3703
268 aagaaaacat tatcccagtt acctacatcg caattacctt atgtaaagca gaactaatgc 3763
270 tgactggatg tttaatggga tgagcattaa agctgcaatc tactatagta ctccagatct 3823
272 ctttcggctt cctatgagaa acaccagaag cactactttc cacttctact tacagtaatt 3883
274 gcaagaggag acctcacatt caggactggc ctagtgaacg taatccatgc tttaaactgg 3943
276 ccattaaaca gtcccacatg gttggatttt tttttttttt ttgagttgtg ctttcacaaa 4003
278 acctgtcaa agacctcatg caatatcact ttgaaagtta ttttctgttt actacacaaa 4063
280 cattgtaata taactgttaa tactatttat atatttgaaa ggtataaaaag gtaggagtta 4123
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284 tgttgcaata caagctaatt ctagctgctc agtaacctct ggagttttta aagggacatt 4243
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292 ccaaattgtc ttcttacact gttgctgaag gtcactctgt acacgtaatg gaaactgatt 4483
294 ttgccaagct cttacaagggt gtttcatcta tcgatggcat ccgcatttgg tatcttttac 4543
296 acttcaacca aaaattttatt aggtattttt caatgctaag tcttgccctt tatttttttaa 4603
298 tttcactgcc aagtttgcag tggttctaag tgaatctgtg ggcatttttag cctgtggtct 4663
300 tgccagatct ttgcgaatta caatgcata atgtctattt attcaatata tgtcatataa 4723
302 tatctatttg gaagaagaaa ctttctcttg tagtgccctc tgacaaagca caatttcccg 4783
304 cctttttttt tttttttgtg aaatgaaaaa aacaaattgt gttttattgc ggtatcaaca 4843
306 atgtgaataa ggattaacat attgtaaatg ttcttttttc catgtaaata aactatcttt 4903
308 gttatcacta agtgataatt aatttttaac ttatgtgcat tgtaggctg ttagaatttt 4963
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313 <210> SEQ ID NO: 2

314 <211> LENGTH: 733

315 <212> TYPE: PRT

316 <213> ORGANISM: Homo sapiens

318 <400> SEQUENCE: 2

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326 35 40 45
328 Gly Ala Val Ala Lys Ala Val Gly Gly Leu Met Ile Pro Val Phe Cys
329 50 55 60
331 Val Val Glu Gln Leu Asp Gly Ser Leu Glu Tyr Asp Asn Arg Glu Glu
332 65 70 75 80
334 His Ala Glu Phe Val Leu Val Arg Lys Asp Val Leu Phe Ser Gln Leu
335 85 90 95
337 Val Glu Thr Ala Leu Leu Ala Leu Gly Tyr Ser His Ser Ser Ala Ala
338 100 105 110
340 Gln Ala Gln Gly Ile Ile Lys Leu Gly Arg Trp Asn Pro Leu Pro Leu
341 115 120 125
343 Ser Tyr Val Thr Asp Ala Pro Asp Ala Thr Val Ala Asp Met Leu Gln
344 130 135 140
346 Asp Val Tyr His Val Val Thr Leu Lys Ile Gln Leu Gln Ser Cys Ser
347 145 150 155 160
349 Lys Leu Glu Asp Leu Pro Ala Glu Gln Trp Asn His Ala Thr Val Arg
350 165 170 175
352 Asn Ala Leu Lys Glu Leu Leu Lys Glu Met Asn Gln Ser Thr Leu Ala
353 180 185 190
355 Lys Glu Cys Pro Leu Ser Gln Ser Met Ile Ser Ser Ile Val Asn Ser
356 195 200 205
358 Thr Tyr Tyr Ala Asn Val Ser Ala Thr Lys Cys Gln Glu Phe Gly Arg
359 210 215 220
361 Trp Tyr Lys Lys Tyr Lys Lys Ile Lys Val Glu Arg Val Glu Arg Glu
362 225 230 235 240
364 Asn Leu Ser Asp Tyr Cys Val Leu Gly Gln Arg Pro Met His Leu Pro
365 245 250 255

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4